

SUPPLEMENTARY MATERIALS

MATERIALS AND METHODS

The human biological samples used in the following experimentation were collected with the expressed consent, free and informed, to the collection and use, of the person from whom the material was taken, according to current legislation.

Plasma sample preparation

Each plasma sample was treated as follows: 5 μL of CH_3CN were added to 50 μL of plasma and vortexed for 1 minute. The procedure was repeated 10 times. Then the sample was centrifuged at 1,500 g for 10 minutes and two 100 μL aliquots of supernatant were treated under normal and denaturation conditions:

- ***Normal conditions***

The aliquot was dried by nitrogen treatment for 1h and, once fully dried, it was re-suspended in 1,000 μL NH_4HCO_3 50 mM buffer. Filtering by using 0.22 μm bacteriological membrane was applied.

No denaturation process was applied. Desalting was obtained using zip-tip cartridge (Millipore, Italy). After filtration, the sample was eluted in 200 μL of CH_3CN (80%), dried by nitrogen treatment for 30 minutes, and re-suspended in 200 μL NH_4HCO_3 50 mM pH 7.8 buffer solution to allow re-folding. Sorbic acid (solution 1%) was added as antibacterial agent.

- ***Denaturation conditions***

The aliquot was dried by nitrogen treatment for 1h and, once fully dried, it was re-suspended in 1,000 μL NH_4HCO_3 50 mM buffer. Filtering by using 0.22 μm bacteriological membrane was applied.

After filtration, the sample was dried by nitrogen treatment for 30 minutes, re-suspended in 200 μL NH_4HCO_3 50 mM pH 7.8 buffer containing 1% SDS. Sorbic acid (solution 1%) was added as antibacterial agent.

Urine sample preparation

Each urine sample was treated as follows: an equivalent volume of bi-distilled water was added, followed by a centrifuge step at 1,500 g for 10 minutes. Aliquots of the supernatant were directly used for the measurements.

Toxin-like peptide identification

All samples have been analysed for the presence of proteins with potential toxic effect by using the cloud ion mobility mass spectrometry (CIMS) coupled with surface activated chemical ionization-Electrospray-NIST (SANIST) Bayesian model database search (SANIST-CIMS) as described in^{1,2}. The basics of this low voltage technology (no-discharge Atmospheric Pressure Chemical Ionization, APCI) has been adopted and used by the U.S. Food and Drug Administration³⁻⁵. The complete 'UniprotKB set of manually reviewed venom proteins and toxins'⁶

(mixed with a subset of not venom proteins and toxins from UniprotKB in order to give a statistical significance to the results) was used as reference protein dataset.

SANIST technology (surface-activated chemical ionization-electrospray-NIST) was used to obtain and compare the proteomic profiles. An Ultimate 3000 UPLC LC (by ThermoFisher) was used to achieve separation of analytes for each sample prior to MS analysis. A reversed phase C-18 LC column (50 × 2.1 mm; particle size, 5 µm; pore size, 100 Å, by Phenomenex, USA) was used. The eluent flow was 0.25 mL/min and the injection volume was 15 µL. The mobile phases were:

A) 0.2% (v/v) formic acid (HCOOH)

B) acetonitrile (CH₃CN).

The elution gradient was: 2% (v/v) of B between 0 and 2 min; 2 to 30% between 2 and 7 min; 30 to 80% between 7 and 9 min; 80% between 9 and 12 min; 80-2% between 12 and 12.1 min. The column was rebalanced with 2% of B between 12.1 and 17 min.

Samples were analysed with an HCT ion trap mass spectrometer (Breme, Germany) coupled to a surface activated chemical ionization (SACI) / ESI source and operated in positive and negative ion mode. Full scan spectra were acquired in the 40-3,500 m/z range for non-targeted metabolomics/proteomics analyses to detect analytes. The same m/z range was used for both discovery studies and selective biomarker studies in order to standardize the instrument response across the SANIST study, primarily in terms of scan rate.

The ion source parameters were:

- ESI capillary voltage: 1500 V
- SACI surface voltage: 47 V
- Desiccant gas: 2 L / min
- Nebulizer gas: 80 psi
- Temperature: 40 °C.

Mass spectrometry on samples was performed with collision-induced dissociation using helium as the collision gas. The ion trap was applied to isolate and fragment the precursor ions (windows of isolation, ± 0.3 m/z; collision energy, 30% of its maximum value, which was 5V peak to peak), and the Orbitrap mass analyser was used to obtain fragments with an extremely accurate m/z ratio (resolution 15,000; m/z error <10 ppm).

Similarity searches

At the time of writing, TBLASTN⁷ was run at the National Center for Biotechnology Information (NCBI) website⁸ with default options and parameters, with the exception of the following ones: max target sequences = 1,000; expect threshold = 100; word size = 3; gap cost existence = 9; gap cost extension = 1; filter of low complexity regions = No. Searches have been performed versus: Nucleotide collection (nr/nt); Reference RNA sequences (refseq_rna); RefSeq Genome Database (refseq_genomes); Whole-genome shotgun contigs (wgs) from metagenomic experiments; Sequence Read Archive (SRA) sequences from metagenomic experiments; Transcriptome Shotgun

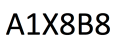
Assembly (TSA); Patent sequences(pat); Human RefSeqGene sequences(RefSeq_Gene); Betacoronavirus Genbank sequence dataset. The information reported in Table 1 has been retrieved from the UniprotKB⁹ database and from the NCBI Taxonomy database¹⁰.

References

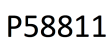
1. Arzoni A, Bernardi LR, Cristoni S. In-source cloud ion mobility mass spectrometry. *Rapid Commun Mass Spectrom* 2015; **29**: 690–4.
2. Cristoni S, Dusi G, Brambilla P, *et al.* SANIST: optimization of a technology for compound identification based on the European Union directive with applications in forensic, pharmaceutical and food analyses. *J Mass Spectrom* 2017; **52**: 16–21.
3. U.S. Food and Drug Administration. Determination and Confirmation of Leucomalachite Green in Salmon using No-Discharge Atmospheric Pressure Chemical Ionization LC-MSn. 2004 <https://www.fda.gov/food/laboratory-methods-food/laboratory-information-bulletin-lib-4333-leucomalachite-green-salmon>.
4. Turnipseed SB, Andersen WC, Roybal JE. Determination and confirmation of malachite green and leucomalachite green residues in salmon using liquid chromatography/mass spectrometry with no-discharge atmospheric pressure chemical ionization. *J AOAC Int*; 88: 1312–7.
5. Turnipseed SB, Andersen WC, Karbiwnyk CM, Roybal JE, Miller KE. No-discharge atmospheric pressure chemical ionization: evaluation and application to the analysis of animal drug residues in complex matrices. *Rapid Commun Mass Spectrom* 2006; 20: 1231–9.
6. UniprotKB. Animal toxin annotation project. <https://www.uniprot.org/program/Toxins> (accessed Oct 4, 2020).
7. Altschul SF, Gish W, Miller W, Myers EW, Lipman DJ. Basic local alignment search tool. *J Mol Biol* 1990; **215**: 403–10.
8. <https://blast.ncbi.nlm.nih.gov/Blast.cgi>
9. <https://www.uniprot.org/>
10. <https://www.ncbi.nlm.nih.gov/taxonomy>

D2DGD8

B3FIA5



Q5K0C5



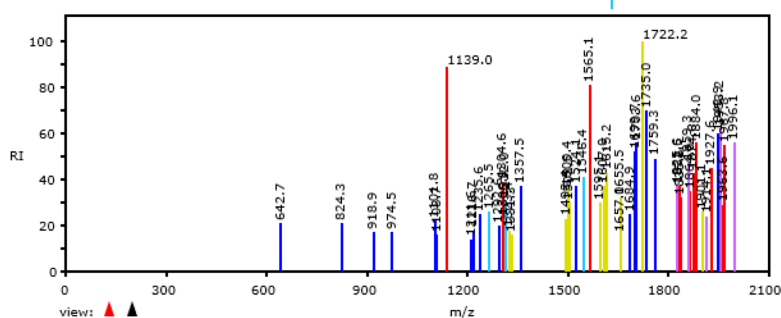
Mass spectrum of compound 10. The x-axis represents the mass-to-charge ratio (m/z) from 0 to 2100, and the y-axis represents the relative intensity (RI) from 0 to 100. The base peak is at m/z 1960.6. Other labeled peaks include:

m/z	Relative Intensity (RI)
729.8	~55
790.5	~45
902.3	~45
955.5	~35
1086.6	~35
1151.4	~35
1176.6	~45
1242.1	~45
1369.8	~45
1490.3	~45
1509.6	~45
1549.3	~45
1619.5	~45
1639.5	~45
1729.5	~45
1769.5	~45
1829.5	~45
1849.5	~45
1869.5	~45
1889.5	~45
1909.1	~45
1929.1	~45
1949.1	~45
1960.6	100

Mass spectrum of compound 10. The x-axis represents the mass-to-charge ratio (m/z) from 0 to 2100, and the y-axis represents the relative intensity (RI) from 0 to 100. The base peak is at m/z 1650.3. Other labeled peaks include:

m/z	Relative Intensity (RI)
627.5	~5
648.3	~10
680.6	~10
690.4	~10
933.2	~5
1053.6	~25
1086.6	~25
1246.3	~20
1275.8	~20
1336.6	~15
1366.4	~10
1471.4	~40
1593.1	~95
1650.3	100
1769.8	~10
1879.4	~10
1944.6	~10

V L A T T G V S F T L D R A S D G G N A V A K K S D V T A R F N W R C C L I P A C R R N H K K F C



RDVCELPIFEELGIPCFAAIR

view: ▲ ▼

MFTVFLLVILATTVPFPFS'DRDPASINHE'NS'KGSNNRAWLTPEEICIAAPACREIMILEFC

view: ▲ ▼

mass spectrum plot showing relative intensity (RI) versus mass-to-charge ratio (m/z). The x-axis ranges from 0 to 3000 m/z, and the y-axis ranges from 0 to 100 RI. The base peak is at m/z 2342.7. Other significant peaks are labeled with their m/z values.

m/z	Relative Intensity (RI)
2342.7	100
2375.5	~5
2382.5	~5
2414.5	~5
2443.2	~5
2459.6	~5
2482.7	~5
2533.6	~5
2562.7	~5
2624.0	~5
2644.9	~5
2652.4	~5
2659.4	~5
2745.7	~5
2758.2	~5
2768.2	~5
2770.2	~5
2771.2	~5
2772.2	~5
2773.2	~5
2774.2	~5
2775.2	~5
2776.2	~5
2777.2	~5
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2783.2	~5
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2801.2	~5
2802.2	~5
2803.2	~5
2804.2	~5
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2862.2	~5
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2906.2	~5
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2916.2	~5
2917.2	~5
2918.2	~5
2919.2	~5
2920.2	~5
2921.2	~5
2922.2	~5
2923.2	~5
2924.2	~5
2925.2	~5
2926.2	~5
2927.2	~5
2928.2	~5
2929.2	

ALGEGDGQAVAGDRNP⁵EARSTHEHFLQR¹L¹RL¹IL¹HGSD¹C¹Q¹PC¹GQYVCCP

view: ▲ ▼

PAHL LVL AAVCI SLSGASSIAPQPLNLI QFGNMI QCTI P GSSP LLDYADY GCIY CIG RGG

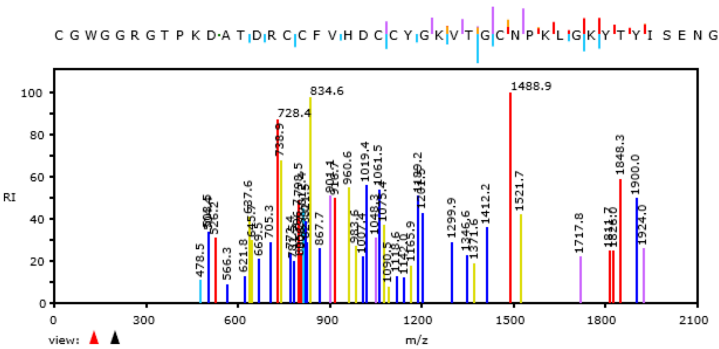
Mass spectrum plot showing relative intensity (RI) versus mass-to-charge ratio (m/z). The x-axis ranges from 0 to 3000 m/z, and the y-axis ranges from 0 to 100 RI. The base peak is at m/z 2872.0. Other significant peaks are labeled with their m/z values.

m/z	Relative Intensity (RI)
1378.6	~5
2154.6	~25
2410.7	~75
2581.7	~45
2654.7	~15
2680.3	~15
2711.4	~15
2744.6	~15
2777.8	~15
2802.0	~15
2822.1	~15
2832.1	~15
2852.1	~15
2872.0	100
2892.1	~15
2912.1	~15
2932.1	~15
2952.1	~15
2972.1	~15
2992.1	~15

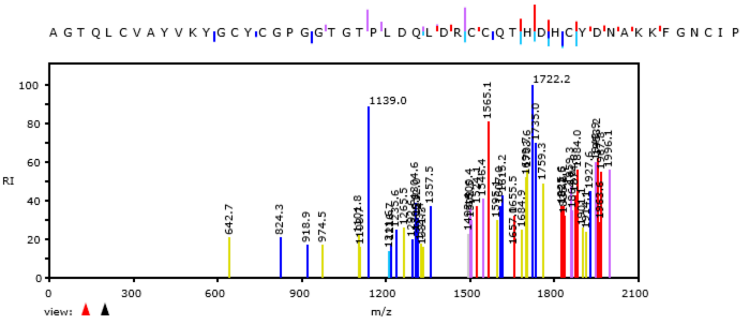
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F L V V I V T T V S L A G A A S A G E I Q N L Y Q F G K

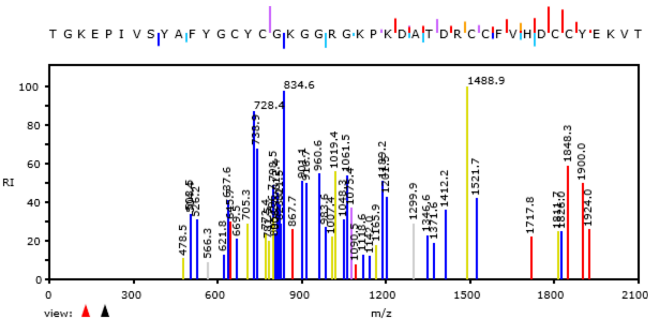
Q2PG83



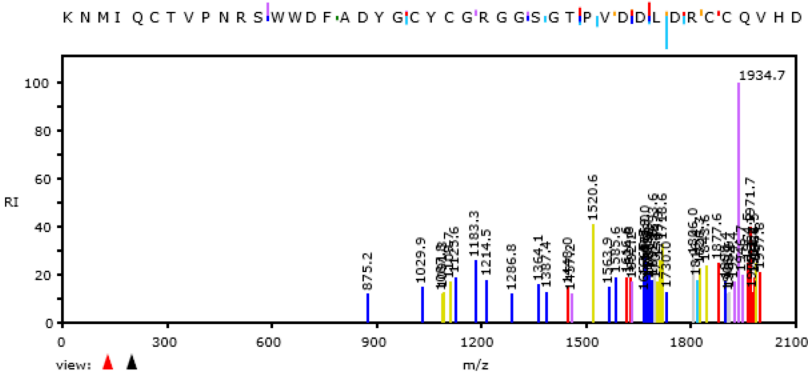
A6MEY4



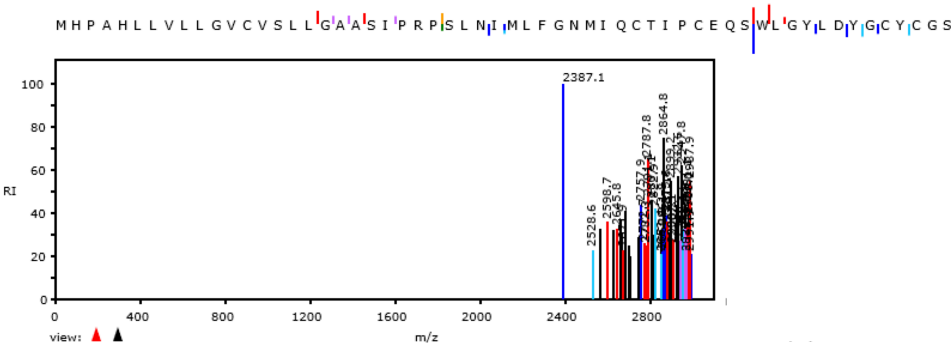
P06860



Q9I900



P23028-1



K P S L Q Y T I N G F A N G T L P D V Q A C A Y D H I S W H L I G M S S S P E I F S V H F N G Q T L E Q N H Y K V S

Mass spectrum plot showing relative intensity (RI) versus mass-to-charge ratio (m/z). The x-axis ranges from 0 to 3000 m/z, and the y-axis ranges from 0 to 100 RI. The base peak is at m/z 2242.8. Other significant peaks are labeled with their m/z values.

m/z	RI (approx)
2242.8	100
2243.8	95
2471.3	35
2642.9	10
2652.9	10
2662.9	10
2672.9	10
2682.9	10
2692.9	10
2702.9	10
2712.9	10
2722.9	10
2732.7	10
2738.7	10
2758.2	10
2766.7	10
2858.1	10
2868.1	10
2878.1	10
2888.1	10
2898.1	10
2908.1	10
2918.1	10
2928.1	10
2938.1	10
2948.1	10
2958.1	10
2968.1	10
2978.1	10
2988.1	10
2998.1	10

view: ▲ ▼

K P S L Q Y T I N G F A N G T L P D V Q A C A Y D H I S W H L I G M S S S P E I F S V H F N G Q T L E I Q N H Y K V S

view: ▲ ▼

m/z	Relative Intensity (RI)
745.5	~75
1795.6	~70
2400.5	~10
2537.6	~10
2538.6	~10
2539.6	~10
2540.6	~10
2541.6	~10
2542.6	~10
2543.6	~10
2544.6	~10
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2648.6	~10
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2681.6	~10
2682.6	~10
2683.6	~10
2684.6	~10
2685.6	~10
2686.6	~10
2687.6	~10
2688.6	~10
2689.6	~10
2690.6	~10
2691.6	~10
2692.6	~10
2693.6	~10
2694.6	~10
2695.3	100
2696.6	~10
2697.6	~10
2698.6	~10
2699.6	~10
2700.6	~10
2701.6	~10
2702.6	~10
2703.6	~10

I A K E L G L L D D E D N Q E E S H N V Q T E D D E E Q L M I A T M L G F R S F K G S V A E E L N L I T A I L A L E E

EVWGFHQSEVVEWHLTSGVTDEIVP-V-H'L S GHT F L S K G K H Q D I L N L F P M S G E I A I T V T M

T C Y K G Y H D T V V C K P H E T I C Y E Y F I P A I T H G N A I L A R G C G T S C P G G I R P V C C

Mass spectrum showing relative intensity (RI) versus mass-to-charge ratio (m/z). The spectrum displays several peaks, with the base peak at m/z 1722.2. Other labeled peaks include m/z 642.7, 824.3, 918.9, 974.5, 1087.8, 1116.1, 1125.6, 1150.6, 1157.5, 1200.4, 1246.9, 1259.2, 1357.5, 1400.4, 1404.4, 1426.9, 1436.2, 1451.5, 1455.5, 1459.2, 1460.6, 1498.2, 1508.3, 1565.1, 1578.0, 1580.3, 1584.0, 1585.3, 1586.6, 1587.9, 1589.2, 1590.5, 1591.8, 1593.1, 1594.4, 1595.7, 1597.0, 1598.3, 1599.6, 1600.9, 1602.2, 1603.5, 1604.8, 1606.1, 1607.4, 1608.7, 1610.0, 1611.3, 1612.6, 1613.9, 1615.2, 1616.5, 1617.8, 1619.1, 1620.4, 1621.7, 1623.0, 1624.3, 1625.6, 1626.9, 1628.2, 1629.5, 1630.8, 1632.1, 1633.4, 1634.7, 1636.0, 1637.3, 1638.6, 1639.9, 1641.2, 1642.5, 1643.8, 1645.1, 1646.4, 1647.7, 1649.0, 1650.3, 1651.6, 1652.9, 1654.2, 1655.5, 1656.8, 1658.1, 1659.4, 1660.7, 1662.0, 1663.3, 1664.6, 1665.9, 1667.2, 1668.5, 1669.8, 1671.1, 1672.4, 1673.7, 1675.0, 1676.3, 1677.6, 1678.9, 1680.2, 1681.5, 1682.8, 1684.1, 1685.4, 1686.7, 1688.0, 1689.3, 1690.6, 1691.9, 1693.2, 1694.5, 1695.8, 1697.1, 1698.4, 1699.7, 1701.0, 1702.3, 1703.6, 1704.9, 1706.2, 1707.5, 1708.8, 1710.1, 1711.4, 1712.7, 1714.0, 1715.3, 1716.6, 1717.9, 1719.2, 1720.5, 1721.8, 1723.1, 1724.4, 1725.7, 1727.0, 1728.3, 1729.6, 1730.9, 1732.2, 1733.5, 1734.8, 1736.1, 1737.4, 1738.7, 1740.0, 1741.3, 1742.6, 1743.9, 1745.2, 1746.5, 1747.8, 1749.1, 1750.4, 1751.7, 1753.0, 1754.3, 1755.6, 1756.9, 1758.2, 1759.5, 1760.8, 1762.1, 1763.4, 1764.7, 1766.0, 1767.3, 1768.6, 1769.9, 1771.2, 1772.5, 1773.8, 1775.1, 1776.4, 1777.7, 1779.0, 1780.3, 1781.6, 1782.9, 1784.2, 1785.5, 1786.8, 1788.1, 1789.4, 1790.7, 1792.0, 1793.3, 1794.6, 1795.9, 1797.2, 1798.5, 1799.8, 1801.1, 1802.4, 1803.7, 1805.0, 1806.3, 1807.6, 1808.9, 1810.2, 1811.5, 1812.8, 1814.1, 1815.4, 1816.7, 1818.0, 1819.3, 1820.6, 1821.9, 1823.2, 1824.5, 1825.8, 1827.1, 1828.4, 1829.7, 1831.0, 1832.3, 1833.6, 1834.9, 1836.2, 1837.5, 1838.8, 1840.1, 1841.4, 1842.7, 1844.0, 1845.3, 1846.6, 1847.9, 1849.2, 1850.5, 1851.8, 1853.1, 1854.4, 1855.7, 1857.0, 1858.3, 1859.6, 1860.9, 1862.2, 1863.5, 1864.8, 1866.1, 1867.4, 1868.7, 1870.0, 1871.3, 1872.6, 1873.9, 1875.2, 1876.5, 1877.8, 1879.1, 1880.4, 1881.7, 1883.0, 1884.3, 1885.6, 1886.9, 1888.2, 1889.5, 1890.8, 1892.1, 1893.4, 1894.7, 1896.0, 1897.3, 1898.6, 1899.9, 1901.2, 1902.5, 1903.8, 1905.1, 1906.4, 1907.7, 1909.0, 1910.3, 1911.6, 1912.9, 1914.2, 1915.5, 1916.8, 1918.1, 1919.4, 1920.7, 1922.0, 1923.3, 1924.6, 1925.9, 1927.2, 1928.5, 1929.8, 1931.1, 1932.4, 1933.7, 1935.0, 1936.3, 1937.6, 1938.9, 1940.2, 1941.5, 1942.8, 1944.1, 1945.4, 1946.7, 1948.0, 1949.3, 1950.6, 1951.9, 1953.2, 1954.5, 1955.8, 1957.1, 1958.4, 1959.7, 1961.0, 1962.3, 1963.6, 1964.9, 1966.2, 1967.5, 1968.8, 1970.1, 1971.4, 1972.7, 1974.0, 1975.3, 1976.6, 1977.9, 1979.2, 1980.5, 1981.8, 1983.1, 1984.4, 1985.7, 1987.0, 1988.3, 1989.6, 1990.9, 1992.2, 1993.5, 1994.8, 1996.1, 1997.4, 1998.7, 1999.0, 2000.3, 2001.6, 2002.9, 2004.2, 2005.5, 2006.8, 2008.1, 2009.4, 2010.7, 2012.0, 2013.3, 2014.6, 2015.9, 2017.2, 2018.5, 2019.8, 2021.1, 2022.4, 2023.7, 2025.0, 2026.3, 2027.6, 2028.9, 2030.2, 2031.5, 2032.8, 2034.1, 2035.4, 2036.7, 2038.0, 2039.3, 2040.6, 2041.9, 2043.2, 2044.5, 2045.8, 2047.1, 2048.4, 2049.7, 2051.0, 2052.3, 2053.6, 2054.9, 2056.2, 2057.5, 2058.8, 2060.1, 2061.4, 2062.7, 2064.0, 2065.3, 2066.6, 2067.9, 2069.2, 2070.5, 2071.8, 2073.1, 2074.4, 2075.7, 2077.0, 2078.3, 2079.6, 2080.9, 2082.2, 2083.5, 2084.8, 2086.1, 2087.4, 2088.7, 2090.0, 2091.3, 2092.6, 2093.9, 2095.2, 2096.5, 2097.8, 2099.1, 2100.4, 2101.7, 2103.0, 2104.3, 2105.6, 2106.9, 2108.2, 2109.5, 2110.8, 2112.1, 2113.4, 2114.7, 2116.0, 2117.3, 2118.6, 2119.9, 2121.2, 2122.5, 2123.8, 2125.1, 2126.4, 2127.7, 2129.0, 2130.3, 2131.6, 2132.9, 2134.2, 2135.5, 2136.8, 2138.1, 2139.4, 2140.7, 2142.0, 2143.3, 2144.6, 2145.9, 2147.2, 2148.5, 2149.8, 2151.1, 2152.4, 2153.7, 2155.0, 2156.3, 2157.6, 2158.9, 2160.2, 2161.5, 2162.8, 2164.1, 2165.4, 2166.7, 2168.0, 2169.3, 2170.6, 2171.9, 2173.2, 2174.5, 2175.8, 2177.1, 2178.4, 2179.7, 2181.0, 2182.3, 2183.6, 2184.9

Mass spectrum plot showing relative intensity (RI) versus mass-to-charge ratio (m/z). The x-axis ranges from 0 to 2100 m/z, and the y-axis ranges from 0 to 100 RI. The spectrum displays several peaks, with the base peak at m/z 1488.9. A legend indicates that red triangles represent the 'view' and black triangles represent the 'reference'.

Sequence: P P K R D T L R N L L K I G T R G Q G G C V P P G G G R C K A N Q A C I T K G G N P G T C G F Q

m/z	RI (view)	RI (reference)
478.5	478.5	560.6
560.6	560.6	560.6
562.6	562.6	562.6
621.8	621.8	637.6
637.6	637.6	637.6
655.3	655.3	705.3
705.3	705.3	705.3
728.4	728.4	728.4
738.5	738.5	738.5
758.5	758.5	758.5
834.6	834.6	834.6
861.7	861.7	861.7
900.6	900.6	900.6
960.6	960.6	960.6
1019.4	1019.4	1019.4
1045.3	1045.3	1045.3
1061.5	1061.5	1061.5
1112.6	1112.6	1112.6
1127.9	1127.9	1127.9
1140.9	1140.9	1140.9
1218.9	1218.9	1218.9
1280.9	1280.9	1280.9
1346.6	1346.6	1346.6
1412.2	1412.2	1412.2
1488.9	1488.9	1488.9
1521.7	1521.7	1521.7
1717.8	1717.8	1717.8
1816.2	1816.2	1816.2
1848.3	1848.3	1848.3
1924.0	1924.0	1924.0
1960.0	1960.0	1960.0

R K S H D N A Q L L T G I N F N G P I T A G L G Y L G G I C N P M Y S A G I V Q D H N K I H H L V A I A

view: ▲ ▲

m/z	RI
642.7	20
824.3	15
918.9	10
974.5	10
1139.0	90
1160.8	15
1212.5	10
1230.5	10
1250.6	10
1265.6	10
1357.5	10
1492.4	15
1507.4	15
1526.2	15
1565.1	15
1641.5	10
1658.9	10
1688.6	10
1722.2	100
1759.3	10
1784.0	10
1804.0	10
1824.0	10
1844.0	10
1864.0	10
1884.0	10
1904.0	10
1924.0	10
1944.0	10
1964.0	10
1984.0	10
2004.0	10
2024.0	10
2044.0	10
2064.0	10
2084.0	10
2104.0	10

ALARDDRGCTRTCTCGGPKCTGTCTCTNSKCGCRYNIVHPFSGWGCGCA

Mass spectrum showing relative intensity (RI) versus mass-to-charge ratio (m/z). The spectrum displays several peaks, with the base peak at m/z 1463.6. Other labeled peaks include m/z 550.8, 560.8, 575.9, 753.3, 769.7, 800.5, 816.5, 832.5, 848.5, 864.5, 880.5, 896.5, 912.4, 1062.3, 1107.8, 1177.5, 1175.3, 1189.5, 1303.2, 1368.2, 1508.4, 1580.1, 1617.8, 1720.1, 1801.4, 1851.4, 1869.9, and 1899.3.

view: ▲ ▼

VLVAAVLLSAQVMVQGGDGDQPADRDAPVPRIDNPGGTIGKFMYLHGCPFPQ

Mass spectrum plot showing relative intensity (RI) versus mass-to-charge ratio (m/z). The x-axis ranges from 0 to 2100 m/z, and the y-axis ranges from 0 to 100 RI. The spectrum shows several peaks, with the base peak at m/z 1722.2. A legend at the bottom indicates 'view: ▲' (red) and '▼' (black).

m/z	RI	View
642.7	100	▲
824.3	10	▲
918.9	10	▲
974.5	10	▲
1080.8	10	▲
1139.0	90	▲
1167.5	10	▲
1180.6	10	▲
1200.6	10	▲
1257.5	10	▲
1492.4	10	▲
1506.1	10	▲
1565.1	10	▲
1641.5	10	▲
1658.9	10	▲
1680.6	10	▲
1722.2	100	▲
1759.3	10	▲
1784.0	10	▲
1804.0	10	▲
1824.0	10	▲
1844.0	10	▲
1864.0	10	▲
1884.0	10	▲
1904.0	10	▲
1924.0	10	▲
1944.0	10	▲
1964.0	10	▲
1984.0	10	▲
2004.0	10	▲
2024.0	10	▲
2044.0	10	▲
2064.0	10	▲
2084.0	10	▲
2104.0	10	▲

Q A I P G G G I P S A V N S R V G G D E K S G R I S L E K R I C R S G K I T C I P R V G P D V C C E R S D C F

Mass spectrum plot showing relative intensity (RI) versus mass-to-charge ratio (m/z). The x-axis ranges from 0 to 2100 m/z, and the y-axis ranges from 0 to 100 RI. The spectrum shows several peaks, with the base peak at m/z 1934.7. A legend at the bottom indicates that red triangles represent 'view:' and black triangles represent 'view:'.

m/z	RI
875.2	100
1029.9	100
1052.5	100
1052.6	100
1183.3	100
1214.3	100
1286.8	100
1354.1	100
1446.20	100
1520.6	100
1561.9	100
1600.0	100
1600.1	100
1600.2	100
1600.3	100
1600.4	100
1600.5	100
1600.6	100
1600.7	100
1600.8	100
1600.9	100
1601.0	100
1601.1	100
1601.2	100
1601.3	100
1601.4	100
1601.5	100
1601.6	100
1601.7	100
1601.8	100
1601.9	100
1602.0	100
1602.1	100
1602.2	100
1602.3	100
1602.4	100
1602.5	100
1602.6	100
1602.7	100
1602.8	100
1602.9	100
1603.0	100
1603.1	100
1603.2	100
1603.3	100
1603.4	100
1603.5	100
1603.6	100
1603.7	100
1603.8	100
1603.9	100
1604.0	100
1604.1	100
1604.2	100
1604.3	100
1604.4	100
1604.5	100
1604.6	100
1604.7	100
1604.8	100
1604.9	100
1605.0	100
1605.1	100
1605.2	100
1605.3	100
1605.4	100
1605.5	100
1605.6	100
1605.7	100
1605.8	100
1605.9	100
1606.0	100
1606.1	100
1606.2	100
1606.3	100
1606.4	100
1606.5	100
1606.6	100
1606.7	100
1606.8	100
1606.9	100
1607.0	100
1607.1	100
1607.2	100
1607.3	100
1607.4	100
1607.5	100
1607.6	100
1607.7	100
1607.8	100
1607.9	100
1608.0	100
1608.1	100
1608.2	100
1608.3	100
1608.4	100
1608.5	100
1608.6	100
1608.7	100
1608.8	100
1608.9	100
1609.0	100
1609.1	100
1609.2	100
1609.3	100
1609.4	100
1609.5	100
1609.6	100
1609.7	100
1609.8	100
1609.9	100
1610.0	100
1610.1	100
1610.2	100
1610.3	100
1610.4	100
1610.5	100
1610.6	100
1610.7	100
1610.8	100
1610.9	100
1611.0	100
1611.1	100
1611.2	100
1611.3	100
1611.4	100
1611.5	100
1611.6	100
1611.7	100
1611.8	100
1611.9	100
1612.0	100
1612.1	100
1612.2	100
1612.3	100
1612.4	100
1612.5	100
1612.6	100
1612.7	100
1612.8	100
1612.9	100
1613.0	100
1613.1	100
1613.2	100
1613.3	100
1613.4	100
1613.5	100
1613.6	100
1613.7	100
1613.8	100
1613.9	100
1614.0	100
1614.1	100
1614.2	100
1614.3	100
1614.4	100
1614.5	100
1614.6	100
1614.7	100
1614.8	100
1614.9	100
1615.0	100
1615.1	100
1615.2	100
1615.3	100
1615.4	100

TAVPLDGGDQPAADRPAAERMQDDIS'SERHPNMFDAVRDCCPLPACP

Mass spectrum showing relative intensity (RI) versus mass-to-charge ratio (m/z). The spectrum displays several peaks, with the base peak at m/z 1193.9. Other labeled peaks include m/z 478.6, 510.0, 524.7, 545.5, 574.1, 674.1, 686.8, 778.1, 806.8, 820.5, 890.3, 910.4, 920.5, 1010.4, 1020.5, 1030.6, 1040.4, 1050.4, 1060.4, 1070.4, 1080.4, 1090.4, 1100.4, 1110.4, 1120.4, 1130.4, 1140.4, 1150.4, 1160.4, 1170.4, 1180.4, 1190.4, 1200.4, 1210.4, 1220.4, 1230.4, 1240.4, 1250.4, 1260.4, 1270.4, 1280.4, 1290.4, 1300.4, 1310.4, 1320.4, 1330.4, 1340.4, 1350.4, 1360.4, 1370.4, 1380.4, 1390.4, 1400.4, 1410.4, 1420.4, 1430.4, 1440.4, 1450.4, 1460.4, 1470.4, 1480.4, 1490.4, 1500.4, 1510.4, 1520.4, 1530.4, 1540.4, 1550.4, 1560.4, 1570.4, 1580.4, 1590.4, 1600.4, 1610.4, 1620.4, 1630.4, 1640.4, 1650.4, 1660.4, 1670.4, 1680.4, 1690.4, 1700.4, 1710.4, 1720.4, 1730.4, 1740.4, 1750.4, 1760.4, 1770.4, 1780.4, 1790.4, 1800.4, 1810.4, 1820.4, 1830.4, 1840.4, 1850.4, 1860.4, 1870.4, 1880.4, 1890.4, 1900.4, 1910.4, 1920.4, 1930.4, 1940.4, 1950.4, 1960.4, 1970.4, 1980.4, 1990.4, 2000.4.

view: ▲ ▼

P58786

